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1	ATGCTGTTCCGGCCCCGGGGCGGTACGGGCAGGGCTGGGGCGCCGGAGGCT	60
1	M L F R A R G P V R G R G W G R P A E A	20
61	CCCCGGGGGGGGCTCGCCGCCCTGGAGCCCCGCCCTGGATTGCTGCTGGCGCTGCC	120
21	P R R G R S P P W S P A W I C C W A L A	40
121	GGCTGCCAGGGGGCTGGGCTGGGACCTGCCCTCCTCCAGCCGCCGTTCCCT	180
41	G C Q A A W A G D L P S S S S R P L P P	60
181	TGCCAGGAGAAAGATTATCACTTGAAATATACTGAATGCTGGCTCCAGGTGG	240
61	C Q E K D Y H F E Y T E C D S S G S R W	80
241	AGAGTTGCCATTCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC	300
81	R V A I P N S A V D C S G L P D P V R G	100
301	AAAGAATGCCACTTCTCTGTGCTCTGGAGAGTATCTAGAAATGAAGAACCAAGGTATGC	360
101	K E C T F S C A S G E Y L E M K N Q V C	120
361	AGTAAGTGTGTGAAGGCACCTATTCTGGCAGTGGCATCAAATTGATGAATGGAT	420
121	S K C G E G T Y S L G S G I K F D E W D	140
421	GAATTGCCGGCAGGATTTCTAACATCGAACATTCACTGGACACTGTGGTGGCCCTCT	480
141	E L P A G F S N I A T F M D T V V G P S	160
481	GACAGCAGGCCAGACGGCTGTAACAACACTCTCTGGATCCCTCGTGAAACTACATAGAA	540
161	D S R P D G C N N S S W I P R G N Y I E	180
541	TCTAACCGTGTACTGCACGGGTCTTGATCTATGCTGTCACCTTAAGAAGTCAGGC	600
181	S N R D D C T V S L I Y A V H L K K S G	200
601	TATGTCTTCTTGAGTACCAAGTATGTCACAAACATCTCTTGAGTTCTTATTCAA	660
201	Y V F F E Y Q Y V D N N I F F E F F I Q	220

**FIG. 1A**

661 AATGATCAGTGCCAGGAGATGGACACCACACTACAAGTGGTAAAACCTACAGACAAT 720  
 221 N D Q C Q E M D T T T D K W V K L T D N 240  
  
 721 GGAGAATGGGCTCTCATTCTGTAAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780  
 241 G E W G S H S V M L K S G T N I L Y W R 260  
  
 781 ACTACAGGCATCCTATGGGTTCTAAGCGGTCAAGCCTGTGCTGGTAAAAAATATCACA 840  
 261 T T G I L M G S K A V K P V L V K N I T 280  
  
 841 ATTGAAGGGTGGCGTACACATCAGAACATGTTTCCTTGCAAGCCAGGCACATTCAAC 900  
 281 I E G V A Y T S E C F P C K P G T F S N 300  
  
 901 AAACCAGGTTCACTGCCAGGTGTCCAGAAACACCTATTCTGAGAAAGGAGCC 960  
 301 K P G S F N C Q V C P R N T Y S E K G A 320  
  
 961 AAAGAATGTATAAGGTGAAAGACGACTCTCAATTTCAGGATCCAGTGAGTGTACAGAG 1020  
 321 K E C I R C K D D S Q F S G S S E C T E 340  
  
 1021 CGCCCTCCCTGTACACAAAAGACTATTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080  
 341 R P P C T T K D Y F Q I H T P C D E E G 360  
  
 1081 AAGACACAGATAATGTACAAGTGGATAGGCCAAATCTGCCGGGAGGATCTCACAGAT 1140  
 361 K T Q I M Y K W I E P K I C R E D L T D 380  
  
 1141 GCTATTAGATTCCCCCTCTGGAGAGAAGAAGGATTGTCCGCCTGCAACCCCTGGATT 1200  
 381 A I R L P P S G E K K D C P P C N P G F 400  
  
 1201 TATAACAATGGATCATCTCTTGCATCCCTGTCCTCTGGAACATTTCAGATGGAACC 1260  
 401 Y N N G S S S C H P C P P G T F S D G T 420  
  
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTGGCTTGAAATATAATGG 1320  
 421 K E C R P C P A G T E P A L G F E Y K W 440

**FIG. 1B**

1321 TGGAATGTCTTCCTGGCAACATGAAAACCTCCTGCTCAATGTTGGAAATTCAAAGTGC 1380  
 441 W N V L P G N M K T S C F N V G N S K C 460

1381 GATGGAATGAATGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGCTGGAGGTTCT 1440  
 461 D G M N G W E V A G D H I Q S G A G G S 480

1441 GACAATGATTACCTGATCTTAAACTTGCAATATCCAGGATTAAACCACCAACATCTATG 1500  
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGTTCTGAACTAGGAAGAACATTGTCTTGAGACCTCTGTTCA 1560  
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTGACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620  
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGTGGAACCAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCACT 1680  
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTACATGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTCATC 1740  
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTATTCTATCACAGCCACTAATGCAGTTGATGGGTGGCGTCC 1800  
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGTTCTGAACACTCGGGTTCATCGTGTCCCCTGCCCT 1860  
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAACCAACCAAGTGCAGGAATGTCCACCTGACACCTAC 1920  
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGGGGCTGGAGTAAA 1980  
 641 L S I H Q V Y G K E A C I P C G P G S K 660

FIG. 1C

DRAFT  
DNA  
SEQUENCE  
REPORT

1981	AACAATCAGGACCATTGGTTGCTATAGTGA	TGCTTTCTACCATGAAAAAGAAAAT	2040
661	N N Q D H S V C Y S D C F F Y H E K E N		680
2041	CAGATTTCGACTATGACTTACCAACCTCAGCAGTGTGGCTCATTAATGA	ATGGCCCC	2100
681	Q I L H Y D F S N L S S V G S L M N G P		700
2101	AGCTTCACCTCCAAAGGAACAAAATCTTCCATTCTCAATATCAGTTATGTGGCAT		2160
701	S F T S K G T K Y F H F F N I S L C G H		720
2161	GAGGGAAAGAAGATGGCTCTGTACCAACAATAACAGACTTACACTAAAAGAAATA		2220
721	E G K K M A L C T N N I T D F T V K E I		740
2221	GTGGCAGGGTCAGATGATTACACAAATTGGTAGGGCATTGTATGCCACTAACAAATT		2280
741	V A G S D D Y T N L V G A F V C Q S T I		760
2281	ATTCCCTCTGAAACTAAGGGTTCCGAGCAGCCTTATCATCACAAATCCATCATTCTGGCA		2340
761	I P S E S K G F R A A L S S Q S I I L A		780
2341	GATACATTCAAGGAGTCACAGTGAAACCACATTGAAAATATTAAATATAAAAAGAAGAT		2400
781	D T F I G V T V E T T L K N I N I K E D		800
2401	ATGTTCCCAGTTCCAACAAGCAAATACCAAGATGTGCATTCTTTATAAGTCTTCTACA		2460
801	M F P V P T S Q I P D V H F F Y K S S T		820
2461	GCAACAAACATCTGTATTAATGGCGATCAACTGCTGTGAAAATGAGGTGTAACTCTACT		2520
821	A T T S C I N G R S T A V K M R C N P T		840
2521	AAATCTGGAGCAGGAGTGATTCAGTCCCCAGCAAGTGCCCAGCAGGTACCTGTGATGGG		2580
841	K S G A G V I S V P S K C P A G T C D G		860
2581	TGTACGTTCTATTCTGTGGAGAGTGCTGAAGCTTGCCTCTGTGTACGGAGCATGAC		2640
861	C T F Y F L W E S A E A C P L C T E H D		880

**FIG. 1D**

2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTCAAGAACCTTGTATGTGTGGAAT 2700  
 881 F H E I E G A C K R G F Q E T L Y V W N 900

2701 GAACTAAATGGTCATTAAAGAATTCTTGCTGAGAAAAAGTTGCCAACCTGTGAA 2760  
 901 E P K W C I K G I S L P E K K L A T C E 920

2761 ACGTTGACTTTGGCTGAAGGTGGAGCCGGTGGGAGCTTTACTGCCGTTTGCTG 2820  
 921 T V D F W L K V G A G V G A F T A V L L 940

2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAGAAAAGAACACCATTGAAAT 2880  
 941 V A L T C Y F W K K N Q K K K K T I L N 960

2881 CTGTTCAACTGAAAACCTCAAGATCCCCAAATATATGAAGAGACAGTGCCTGAGCCTGA 2940  
 961 L F N \* 964

2941 GACTAATGAACAAAGAAACCTGCTCTAGTTTACAGGACCATATTTAGGGCTGTCCTC 3000

3001 ATACCTGTCACATTGGTGTCTCACAGAGGAGGGCATGCCGTGAAAGGGAAGGAGAT 3060

3061 TGAAACATTGATTGCCCTATCACATGGTCAACTACCTGCCAAATAAGGAAAGCAAAT 3120

3121 GATTGGGTCTCAACTGAAGATGAAGCTCAACTCAGGAAGAGATTATCTGTATATACAC 3180

3181 ATAATGAAAACCAAGTTAACCCACCAATGCACTGCTGATGCCATATAATTAAAT 3240

3241 GGGTAACTTTATTCTTATGATGTCTACATAACAAGTGTGATTGGAAAGGCACATGTGA 3300

3301 GCATATGCATTATGATCCAATTATGTTTTCTTGTATATTGGGAAATTAAA 3360

3361 ATTTTTTAAGGTAAAAAAAAAAAAAAA 3390

**FIG. 1E**

FIG. 2A

	10	20	30	
1	M L F R A R G P V R G R G I G W G R P A E A P R R G R S P P W S			TR16.aa
1	M	- - - - - D I K N L - L T V	- - -	EMB CAB41042.1 TNFR
1	M	- - - - - C V G A R R L G R G P	- - -	emb CAA53576.1 OX40
	40	50	60	
31	P A W I C C W A L A G C Q A A W A G D L P S S S S R P L P P			TR16.aa
10	- - - - - C T I F Y I T T L A T A D	- - -	-	EMB CAB41042.1 TNFR
13	- - - - - C A A L L L L G L G L S T	- - -	-	emb CAA53576.1 OX40
	70	80	90	
61	C Q E K D Y H F E Y T E C I D S S G S R W R V A I P N S A V D			TR16.aa
23	- - - - - I P T T S S L P	- - -	-	EMB CAB41042.1 TNFR
26	- - - - - V - - T G L H	- - -	-	emb CAA53576.1 OX40
	100	110	120	
91	C S G I P D P V R G K E C T F S C A S G E Y L E M K N Q V C			TR16.aa
30	- - - - - H A E V N G	- - - - - A C D E G E Y L D K R H N Q C	- - -	EMB CAB41042.1 TNFR
31	- - - - - C V G D T Y - - P S N D R C	- - -	-	emb CAA53576.1 OX40
	130	140	150	
121	S K C G E G T Y S L G S G I K F D E W D E L P A G F S N I A			TR16.aa
51	- - - - -	- - - - -	-	EMB CAB41042.1 TNFR
43	- - - - -	- - - - -	-	emb CAA53576.1 OX40
	160	170	180	
151	T F M D T V V G P S D S R P D G C N N S S W I P R G N V I E			TR16.aa
51	- - - - -	- - - - -	-	EMB CAB41042.1 TNFR
43	- - - - -	- - - - -	-	emb CAA53576.1 OX40
	190	200	210	
181	S N R D D C T V S L I Y A V H L K K S G Y V F F E Y Q Y V D			TR16.aa
51	- - - - -	- - - - -	-	EMB CAB41042.1 TNFR
43	- - - - -	- - - - -	-	emb CAA53576.1 OX40
	220	230	240	
211	N N I F F E F F F I Q N D Q C Q E M D T T D K W V K L T D N			TR16.aa
51	- - - - -	- - - - -	-	EMB CAB41042.1 TNFR
43	- - - - -	- - - - -	-	emb CAA53576.1 OX40
	250	260	270	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A			TR16.aa
51	- - - - -	- - - - -	-	EMB CAB41042.1 TNFR
43	- - - - -	- - - - -	-	emb CAA53576.1 OX40
	280	290	300	
271	V K P V L V K N I T I E G V A Y T S E C F P C K P G T F S N			TR16.aa
51	- - - - - C N Q C P P G E F A K	- - -	-	EMB CAB41042.1 TNFR
43	- - - - - C H E C R P G N G M V	- - -	-	emb CAA53576.1 OX40
	310	320	330	
301	K P G S F N C O V C P R N T V S E K G A K E C I R C K D D S			TR16.aa
62	- - - - - V R C N	- - -	-	EMB CAB41042.1 TNFR
54	- - - - - S R C S	- - -	-	emb CAA53576.1 OX40

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FIG. 2B

331	<b>Q F S G S S E C T E R P P C T T K D Y F Q I H T P C D E E G</b>	340	350	360	TR16.aa
66	- - - - -			EMB	CAB41042.1 TNFR
58	- - - - -			emb	CAA53576.1 OX40
		370	380	390	
361	<b>K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K</b>				TR16.aa
66	- - - - -		G N D N	EMB	CAB41042.1 TNFR
58	- - - - -		R S Q N	emb	CAA53576.1 OX40
		400	410	420	
391	<b>K D C P P C N P G F Y N N G S S S C H P C P P G T F S D G T</b>				TR16.aa
70	T K C E R C P P H T Y T A - I P N Y S N G C - - - - -			EMB	CAB41042.1 TNFR
62	T V C R E C G P G F Y N D V V S - S K P C - - - - -			emb	CAA53576.1 OX40
		430	440	450	
421	<b>K E C R P C P A G T E P A L G F E Y K W W W N V L P G N M K T</b>				TR16.aa
91	H Q C R K C - - P T G S - - - - -		F D K V	EMB	CAB41042.1 TNFR
82	K P C T W C N L R S G S - - - - -		E R K Q	emb	CAA53576.1 OX40
		460	470	480	
451	<b>S C F N V G N S K C D G M N G W E V A G D H I Q S G A G G S</b>				TR16.aa
105	K C T G T Q N S K C S C L P G W Y C A T D S S Q T - - - - -			EMB	CAB41042.1 TNFR
98	L C T A T Q D T V C R C R A G - - - T Q P L D S - - - - -			emb	CAA53576.1 OX40
		490	500	510	
481	<b>D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R</b>				TR16.aa
130	- - - - - E D - - - - -			EMB	CAB41042.1 TNFR
119	- - - - - Y K P - - - - -			emb	CAA53576.1 OX40
		520	530	540	
511	<b>I T F V F E T L C S A D C V L Y F M V D I N R K S T N V V E</b>				TR16.aa
132	- - - - - C R D C I - - - - -			EMB	CAB41042.1 TNFR
122	- - - - - G V D C A - - - - -			emb	CAA53576.1 OX40
		550	560	570	
541	<b>S W G G T K E K Q A Y T H I I F K N A T F T F T W A F Q R T</b>				TR16.aa
137	- - - - - - - - - - -			EMB	CAB41042.1 TNFR
127	- - - - - - - - - - -			emb	CAA53576.1 OX40
		580	590	600	
571	<b>N O G O D N R R F I N D M V K I Y S I T A T N A V D G V A S</b>				TR16.aa
137	- - - - - P K R R - - - - -			EMB	CAB41042.1 TNFR
127	- - - - - P - - - - -			emb	CAA53576.1 OX40
		610	620	630	
601	<b>S C R A C A L G S E O S G S S C V P C P P G H Y I E K E T N</b>				TR16.aa
141	- - - - - - - - - - - C P C G Y F - - - - -			EMB	CAB41042.1 TNFR
128	- - - - - - - - - - - C P P G H F - - - - -			emb	CAA53576.1 OX40

FIG. 2C

BIOLOGICAL EFFECT

631 Q C K E C P P D T Y L S P H Q V Y G K E A C I P C G P G S K 147 - - - - - 134 - - - - -	640                    650                    660                                             TR16.aa	G G I EMB CAB41042.1 TNFR S P G emb CAA53576.1 OX40
661 N N O D H S V C Y S D C F F Y H E K E N Q I L H Y D F S N L 150 D E Q G N P I C 137 D N O A C	670                    680                    690                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40
691 S S V G S L M N G P S F T S K G T K Y F H F F N I S L C G H 158 - - - - - K S 142 - - - - - K P W T N	700                    710                    720                                             TR16.aa	C C V EMB CAB41042.1 TNFR C T L emb CAA53576.1 OX40
721 E G K K M A L C T N N I T D F T V K E I V A G S D D Y T N L 163 G E - - - - - 150 A G K H - - - - -	730                    740                    750                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40
751 V G A F V C O S T I I P S E S K G F R A A L S S O S I I L A 166 C D - - - - - 166 C E D R D P E A T Q P Q E T Q G P P A R P I T V Q	760                    770                    780                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40
781 D T F I G V T V E T T L K N I N I K E D M F P V P T S O I P 168 - - - - - 191 P T - - - - -	790                    800                    810                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40
811 D V H F F Y K S S T A T T S C I N G R S T A V K M R C N P T 168 - - - - - 203 S T R P V E V P G G R A V A A I L - - - - -	820                    830                    840                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40
841 K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A 168 - - - - - 220 G L G L V - - - - -	850                    860                    870                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40
871 E A C P L C T E R D F H E I E G A C K T G F O E T L Y V W N 168 - - - - - 229 G P L - - - - -	880                    890                    900                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40
901 E P K W C I K G I S L P E K K L A T C E T V D F W L K V G A 170 - - - - - R N Y R L D P - - - - - 242 - - - - - R D Q R L P P D A H K P - - - - -	910                    920                    930                                             TR16.aa	EMB CAB41042.1 TNFR emb CAA53576.1 OX40

## FIG. 2D

940                    950                    960

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931 **G V G A E T A V I L V A I D T C Y F W K K N Q K K K K T I L N** TR16.aa  
 177 **- - - - F - - - - - - - - - - P P C K L S** EMB | CAB41042.1 TNFR  
 255 **G G G S F R T P I - - - - - Q E E Q A D A H S T L A** emb | CAA53576.1 OX40

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961 **L F N**   
 184 K C - N  
 276 K I

TR16.aa  
 EMB | CAB41042.1 TNFR  
 emb | CAA53576.1 OX40

TR16.aa

PROTEIN SEQUENCES

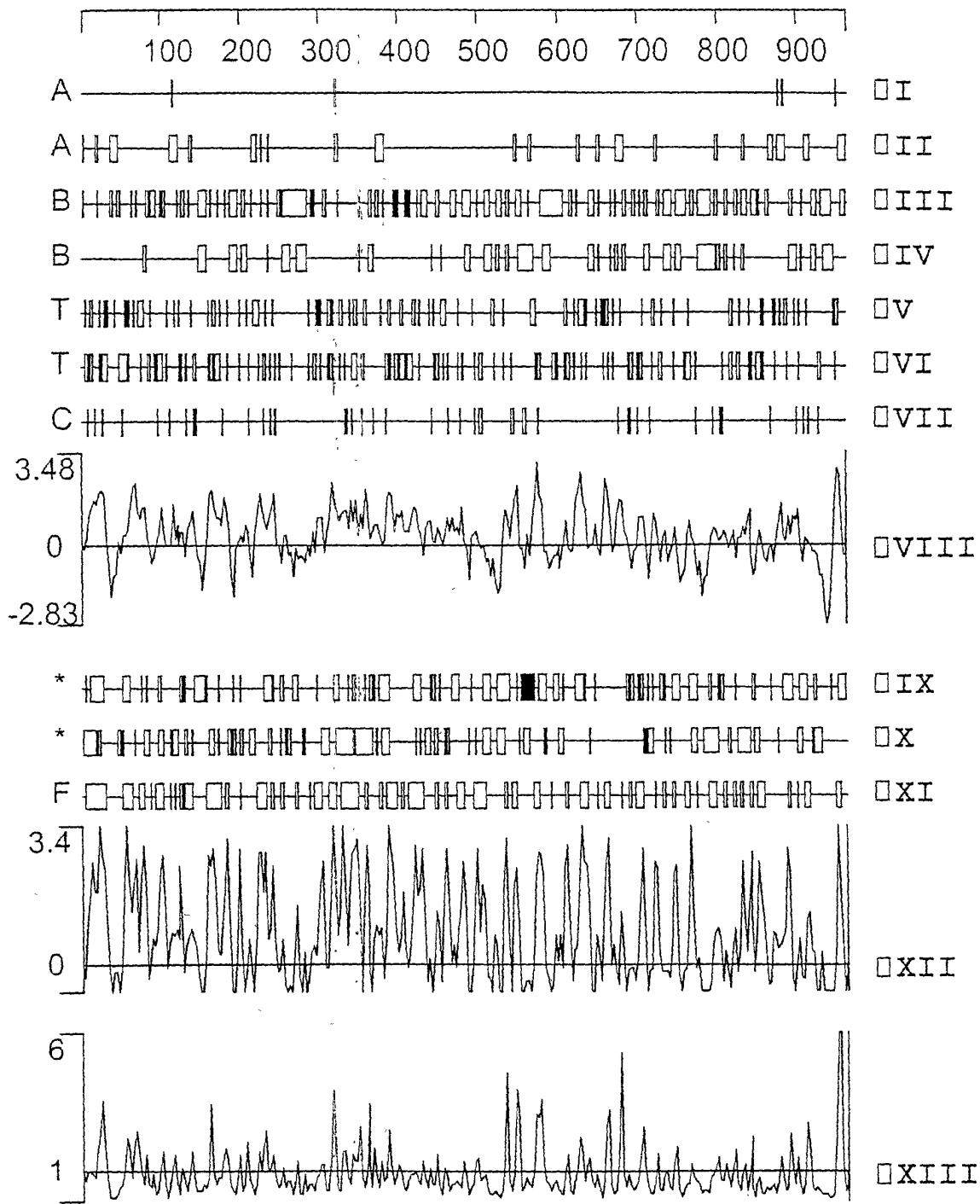


FIG. 3

1 ATGCTGTTCCGCCCGGGGGCGGTACGGGGCAGGGGCTGGGGCGGCCGGAGGCT 60  
 1 M L F R A R G P V R G R G W G R P A E A 20

61 CCCCGCCCGGGGGCTCGCCGUCCCTGGAGCCCCCCTGGATTTGCTGCTGGCGCTGCC 120  
 21 P R R G R S P P W S P A W I C C C W A L A 40

121 GGCTGCCAGGCCCTGGCTGGGACCTGCCCTCCTCCAGCCGCCGCTTCCTCC 180  
 41 G C Q A A W A G D L P S S S S R P L P P 60

181 TGCCAGGAGAAAGATTATCACTTGAATATAACCGAATGTGATAGCAGTGGCTCCAGGTGG 240  
 61 C Q E K D Y H T E Y T E C D S S S G S R W 80

241 AGAGTTGCCATTCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300  
 81 R V A I P N S A W D C S G L P D P V R G 100

301 AAAGAATGCACTTCTCTGTGCTCTGGAGACTATCTAGAAATGAACAACCAGGTATGC 360  
 101 K E C T F S C A S G E Y L E M K N Q V C 120

361 AGTAAGTGTGGTGAAGGCACCTATTCTGGCAGTGGCATCAAATTGATGAATGGGAT 420  
 121 S K C G E G T Y S L G S G I K F D E W D 140

421 GAATTGCCGGCAGGATTTCATAACATCGAACATTCATGGACACTGTGGTGGGCCCTCT 480  
 141 E L P A G F S N I A T F M D T V V G P S 160

481 GACAGCAGGCCAGACGGCTGTAACAACCTTCTGGATCCCTCGTGGAAACTACATAGAA 540  
 161 D S R P D G C N N S S W I P R G N Y I E 180

541 TCTAACGTGATGACTGCACGGTGTCTTGATCTATGCTGTGACCTTAAGAAGTCAGGC 600  
 181 S N R D D C T V S L I Y A V H L K K S G 200

601 TATGCTTCTTGAGTACCAAGTATGTCGACAACAACATCTCTTGAGTTCTTATTCAA 660  
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

661 AATGATCAGTGCAGGAGATGGACACCACCTGACAAGTGGTAAAACCTACAGACAAT 720  
 221 N D Q C Q E M D T T T D K W V K L T D N 240

FIG. 4A

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721	GGAGAATGGGGTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA	780
241	G E W G S H S V M L K S G T N I L Y W R	260
781	ACTACAGGCATCCTTATGGGTCTAAGGCGGTCAAGCCTGTGGTAAAAATATCACA	840
261	T T G I L M G S K A V K P V L V K N I T	280
841	ATTGAAGGGTGGCGTACACATCAGAATGTTTCTTGCAGGCCAGGCACATTAGCAAC	900
281	I E G V A Y T S E C F P C K P G T F S N	300
901	AAACCAGGTTCAATTCAACTGCCAGGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC	960
301	K P G S F N C Q Y C P R N T Y S E K G A	320
961	AAAGAATGTATAAGGTGAAAGACGACTCTCAATTTCAGGATCCAGTGAGTGTACAGAG	1020
321	K E C I R C K D D S Q F S G S S E C T E	340
1021	CGCCCTCCCTGTACCAACAAAAGACTATTCCAGATCCATACTCCATGTGATGAAGAAGGA	1080
341	R P P C T T K D Y F Q I H T P C D E E G	360
1081	AAGACACAGATAATGTACAAGTGGATAGAGCCCCAAATCTGCCGGGAGGATCTCACAGAT	1140
361	K T Q I M Y K W I E P K I C R E D L T D	380
1141	GCTATTAGATTGCCCTTCTGGAGAGAAGAAGGATTGTCCCTTGCAACCTGGATT	1200
381	A I R L P P S G E K K D C P P C N P G F	400
1201	TATAACAATGGATCATCTTCTTGCATCCCTGTCCCTGGAACATTTCAGATGGAACC	1260
401	Y N N G S S S C H P C P P G T F S D G T	420
1261	AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGTTGAATATAATGG	1320
421	K E C R P C P A G T E P A L G F E Y K W	440
1321	TGGAATGTCTTCTGGCAACATGAAAACCTCCTGCTCAATGTTGGAAATTCAAAGTGC	1380
441	W N V L P G N M K T S C F N V G N S K C	460
1381	GATGGAATGAATGGTGGGAGGTCGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT	1440
461	D G M N G W E V A G D H I Q S G A G G S	480

FIG. 4B

1441	GACAATGATTACCTGATCTTAAACTGCATATCCCAGGATTAAACCACCAACATCTATG	1500
481	D N D Y L I L N L H I P G F K P P T S M	500
1501	ACTGGAGCCACGGGTCTGAACTAGGAAGAATAACATTTGCTTGAGACCTCTGTTCA	1560
501	T G A T G S E L G R I T F V F E T L C S	520
1561	GCTGACTGIGTTTGACTTCATGGTGGATATTAAATAGAAAAAGTACAAATGTGGTAGAA	1620
521	A D C V L Y F M V D I N R K S T N V V E	540
1621	TCGTGGGTGGAACCAAAGAAAAACAAGCTTACACCCATATCATCTCAAGAACATGCAACT	1680
541	S W G G T K E K Q A Y T H I I F K N A T	560
1681	TTTACATTTACATGGCATTCCAGAGAACTAATCAGGTCAAGATAATAGACGGTTCATC	1740
561	F T F T W A F Q R T N Q G Q D N R R F I	580
1741	AATGACATGGTAAGATTATTCTATCACAGCCACTAATGCAGTTGATGGGTGGCGTCC	1800
581	N D M V K I Y S I T A T N A V D G V A S	600
1801	TCATGCCGTGCCCTGCCCCCTGGTCTGAACAGTCGGTTCATCGTGTGTCCTGCCCT	1860
601	S C R A C A L G S E Q S G S S C V P C P	620
1861	CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGCAAGGAATGTCCACCTGACACCTAC	1920
621	P G H Y I E K E T N Q C K E C P P D T Y	640
1921	CTGTCCATACATCAGGTCTATGGAAAGAGGTTGTATTCCATGCCGCTGGAGTAAA	1980
641	L S I H Q V Y G K E A C I P C G P G S K	660
1981	AAACATCAGGACCATTGGTCTGCTATAGTGACTGCTTTCTACCATGAAAAAGAAAAT	2040
661	N N Q D H S V S Y S D C F F Y H E K E N	680
2041	CAGATTTCACCTCCAAGGAACAAATACTTCCATTCTCAATATCAGTTATGTGGCAT	2100
681	Q I L H Y D F S N L S S V G S L M N G P	700
2101	AGCTTCACCTCCAAGGAACAAATACTTCCATTCTCAATATCAGTTATGTGGCAT	2160
701	S F T S K G T K Y F H F F N I S L C G H	720

2161	GAGGGGAAGAAGATGGCTCTGTACCAACAATAACAGACTTACAGTAAAGAAATA	2220
721	E G K K M A L C T N N I T D F T V K E I	740
2221	GTGGCAGGGTCAGATGATTACACAAATTGGTAGGGCATTTGTATGCCAGTCAACAATT	2280
741	V A G S D D Y T N L V G A F V C Q S T I	760
2281	ATTCTCTGAAAGTAAGGTTCCGAGCAGCCTTATCATCACAAATCCATCATTCTGGCA	2340
761	I P S E S K G F R A A L S S Q S I I L A	780
2341	GATACATTCA TAGGAGTCACAGTGAAACCACATTGAAAAATTTAATATAAAAAGAAGAT	2400
781	D T F I G V T V E T T L K N I N I K E D	800
2401	ATGTTCCCAGTTCCAACAAGCTAAATACCAAGATGTGCATTCTTTATAAGTCTTCTACA	2460
801	M F P V P T S Q I P D V H F F Y K S S T	820
2461	GCAACAACATCTTGATTAAATGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT	2520
821	A T T S C I N G R S T A V K M R C N P T	840
2521	AAATCTGGAGCAGGAGTGATTCAGTCCCCAGCAAGTGCCAGCAGGTACCTGTGATGGG	2580
841	K S G A G V I S V P S K C P A G T C D G	860
2581	TGTACGTTCTATTCTGTGGGAGAGTGCAGCTGCCCTCTGTGTACGGAGCATGAC	2640
861	C T F Y F L W E S A E A C P L C T E H D	880
2641	TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTCAGGAAACCTTGTATGTGTGGAAT	2700
881	F H E I E G A C K R G F Q E T L Y V W N	900
2701	GAACCTAAATGGTCATTAAAGGAAATTCTTGCTGAGAAAAAGTGGCAACCTGTGAA	2760
901	E P K W C I K G I S L P E K K L A T C E	920
2761	ACGGTTGACTTTGGCTGAAGGTGGAGCCGGTGGGAGCTTTACTGCCGTTTGCTG	2820
921	T V D F W L K V G A G V G A F T A V L L	940
2821	GTGGCTCTGACCTGCTACTTCTGGAAAAAGAATCAAAAATGGAATACAAATATTCCAAG	2880
941	V A L T C Y F W K K N Q K L E Y K Y S K	960

**FIG. 4D**

2881	TTAGTAATGACGACTAACTCAAAAGAGTGTGAACCTCCGGCTGCAGACAGTTGTGCTATC	2940
961	L V M T T N S K E C E L P A A D S C A I	980
2941	ATGGAAGGAGAACATAATGAACAGGAAGTGTATATTCCAATAAACAGTCACTACTAGGA	3000
981	M E G E D N E S E V V Y S N K Q S L L G	1000
3001	AAACTCAAATCTTGGCAACCAAGGAAAAGAAGACCATTGAACTCTGTCAACTGAAA	3060
1001	K L K S L A T K E K E D H F E S V Q L K	1020
3061	ACCTCAAGATCCCCAAATATATGAAGAGACAGTGCTGTAGCCTTGAGACTAATGAACAAA	3120
1021	T S R S P N I *	1028
3121	GAAACCTGCTCTAGTTTACAGGACCATATTTAGGGTCTGCCTCATACCTGTCACATT	3180
3181	GGTGATCTCACAGAGGAGGGCATGCCGCTAAAAGGAAGGAGATTGAAACATTGATT	3240
3241	GCCTTATCACATGGTCAAGTACCTGCCAATAAGGAAGCAAATGATTGGGTCTCAA	3300
3301	CTGAAGATGAAGCTCAACTCAGGAAGAGATTATCTGTATATAACACATAACTGAAAACCA	3360
3361	AGTTTAAGCCCACCAATGCCACTGCTCATGCCATATAATTAAATGGTAACTTTATT	3420
3421	CTTTATGATGTCTACATAACAAGTGTGATTGGAAGGCACATGTGAGCATATGCATTATG	3480
3481	ATCCAATTATGTTTTCTTGTATATTGGGAAATTAAAATTTTTAAGGTA	3540
3541	AAAAAAAAAAAAAAA 3556	

**FIG. 4E**

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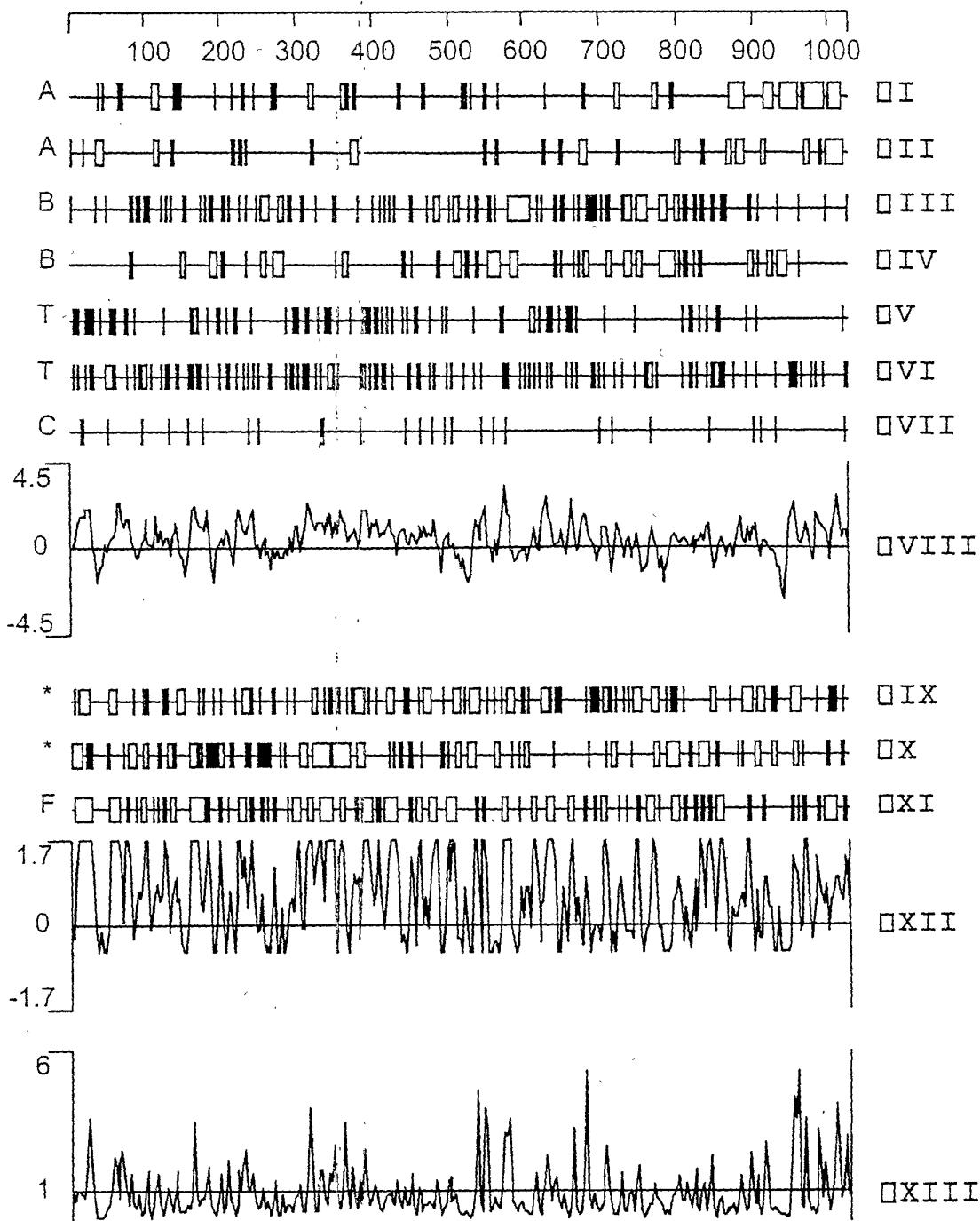


FIG. 5

	10	20	30	40
1	MLFRARGPVRGRGWRPAEAPRRGRSPPWSPA	WICCWALA	SEQ ID 2	
1	----- SEC10			
	50	60	70	80
41	GCQAAWAGDLPSSSRPLPPCQEKDYHF	EYTECDSSGSRW	SEQ ID 2	
1	----- SEC10			
	90	100	110	120
81	RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLEMKNQVC	MKNQVC	SEQ ID 2	
1	----- MKNQVC SEC10			
	130	140	150	160
121	SKCGEGTYSLGSGIKFDEWDELPGFSNIATFM	D T V V G P S	SEQ ID 2	
7	SKCGEGTYSLGSGIKFDEWDELPGFSNIATFM	D T V V G P S	SEC10	
	170	180	190	200
161	DSRPDGCNNSSWI PRGNYIESNRDDCTVSLIYAVHLKKSG	SEQ ID 2		
47	DSRPDGCNNSSWI PRGNYIESNRDDCTVSLIYAVHLKKSG	SEQ10		
	210	220	230	240
201	YVFFEYQYVDNNIFFEFFIQNDQCQEMDTT	T D K W V K L T D N	SEQ ID 2	
87	YVFFEYQYVDNNIFFEFFIQNDQCQEMDTT	T D K W V K L T D N	SEC10	
	250	260	270	280
241	GEWGSHSVMLKSGTNILYWR	TTGILMGSKAVKPVLVKNIT	SEQ ID 2	
127	GEWGSHSVMLKSGTNILYWR	TTGILMGSKAVKPVLVKNIT	SEC10	
	290	300	310	320
281	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A	SEQ ID 2		
167	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A	SEC10		
	330	340	350	360
321	K E C I R C K D D S Q F S	-- GSSECTERPPCTTKDYFQIHTPCDE	SEQ ID 2	
207	K E C I R C K D D S Q F S	SEE GSSECTERPPCTTKDYFQIHTPCDE	SEC10	
	370	380	390	400
359	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P	SEQ ID 2		
247	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P	SEQ10		
	410	420	430	440
399	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y	SEQ ID 2		
287	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y	SEC10		
	450	460	470	480
439	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G	SEQ ID 2		
327	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G	SEC10		
	490	500	510	520
479	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L	SEQ ID 2		
367	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L	SEC10		

FIG. 6A

530	540	550	560
519 C S A D C V L Y F M V D I N R K S T N V V E S W G G T K E K Q A Y T H I I F K N			SEQ ID 2
407 C S A D C V L Y F M V D I N R K S T N V V E S W G G T K E K Q A Y T H I I F K N			SEC10
<hr/>			
570	580	590	600
559 A T F T F T W A F Q R T N Q G Q D N R R F I N D M V K I Y S I T A T N A V D G V			SEQ ID 2
447 A T F T F T W G I P R E - - - - -			SEC10
<hr/>			
610	620	630	640
599 A S S C R A C A L G S E Q S G S S C V P C P P G H Y I E K E T N Q C K E C P P D			SEQ ID 2
459 - - - - -			SEC10
<hr/>			
650	660	670	680
639 T Y L S I H Q V Y G K E A C I P C G P G S K N N Q D H S V C Y S D C F F Y H E K			SEQ ID 2
459 - - - - -			SEC10
<hr/>			
690	700	710	720
659 E N Q I L H Y D F S N L S S V G S L M N G P S F T S K G T K Y F H F F N I S L C			SEQ ID 2
459 - - - - - L I Q G P R			SEC10
<hr/>			
730	740	750	760
719 G H E G K K M A L C T N N I T D F T V K E I V A G S D D Y T N L V G A F V C Q S			SEQ ID 2
464 - - - - -			SEC10
<hr/>			
770	780	790	800
759 T I I P S E S K G F R A A L S S Q S I I L A D T F I G V T V E T T L K N I N I K			SEQ ID 2
464 - - - - -			SEC10
<hr/>			
810	820	830	840
799 E D M F P V P T S Q I P D V H F F Y K S S T A T T S C I N G R S T A V K M R C N			SEQ ID 2
464 - - - - -			SEC10
<hr/>			
850	860	870	880
839 P T K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A E A C P L C T E			SEQ ID 2
464 - - - - -			SEC10
<hr/>			
890	900	910	920
879 H D F H E I E G A C K R G F Q E T L Y V W N E P K W C I K G I S L P E K K L A T			SEQ ID 2
464 - - - - -			SEC10
<hr/>			
930	940	950	960
919 C E T V D F W L K V G A G V G A F T A V L L V A L T C Y F W K K N Q K K K K T I			SEQ ID 2
464 - - - - -			SEC10
<hr/>			
959 L N L F N			SEQ ID 2
464 - - - - -			SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B

	10	20	30	40	
1	MLF R A R G P V R G R G W G R P A E A P R R G R S P P W S P A W I C C W A L A				SEQ ID 4 SEC10
1	-----				
	50	60	70	80	
41	G C Q A A W A G D L P S S S S R P L P P C Q E K D Y H F E Y T E C D S S G S R W				SEQ ID 4 SEC10
1	-----				
	90	100	110	120	
81	R V A I P N S A V D C S G L P D P V R G K E C T F S C A S G E Y L E M K N Q V C				SEQ ID 4 SEC10
1	-----				
	130	140	150	160	
121	S K C G E G T Y S L G S G I K F D E W D E L P A G E F S N I A T F M D T V V G P S				SEQ ID 4 SEC10
7	S K C G E G T Y S L G S G I K F D E W D E L P A G E F S N I A T F M D T V V G P S				
	170	180	190	200	
161	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEQ ID 4 SEC10
47	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				
	210	220	230	240	
201	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D K W V K L T D N				SEQ ID 4 SEC10
87	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D K W V K L T D N				
	250	260	270	280	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K P V L V K N I T				SEQ ID 4 SEC10
127	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K P V L V K N I T				
	290	300	310	320	
281	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				SEQ ID 4 SEC10
167	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				
	330	340	350	360	
321	K E C I R C K D D S Q F S - G S S E C T E R P P C T T K D Y F Q I H T P C D E				SEQ ID 4 SEC10
207	K E C I R C K D D S Q F S E E G S S E C T E R P P C T T K D Y F Q I H T P C D E				
	370	380	390	400	
359	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				SEQ ID 4 SEC10
247	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				
	410	420	430	440	
399	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEQ ID 4 SEC10
287	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				
	450	460	470	480	
439	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEQ ID 4 SEC10
327	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				
	490	500	510	520	
479	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L				SEQ ID 4 SEC10
367	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L				

FIG. 7A

B D C E F G H E P S T R Q K N D Y V I M A L C T N N I T D F T V K E I V A G S D D Y T N L V G A F V C Q S

	530	540	550	560	
519	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN				SEQ ID 4
407	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN				SEC10
	570	580	590	600	
559	ATFTFTWAFQRTTNQGQDNRRFINDMVVKIYSITATNAVDGV				SEQ ID 4
447	ATFTFTWGIPIRE-----				SEC10
	610	620	630	640	
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKEETNQCKECPD				SEQ ID 4
459	-----				SEC10
	650	660	670	680	
639	TYLSIHQVYGKEACIPCGPGSKNNQDHHSVVCYSDCFFYHEK				SEQ ID 4
459	-----				SEC10
	690	700	710	720	
679	ENQILHYDFSNLSSVGSLMNGPSFTSKGTKYFHFFNISLC				SEQ ID 4
459	-----LIQGP-----				SEC10
	730	740	750	760	
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS				SEQ ID 4
464	-----				SEC10
	770	780	790	800	
759	TIIPSSESKGFRALAQSIIADTFIGVTVEETTLKNINI				SEQ ID 4
464	-----				SEC10
	810	820	830	840	
799	EDMFPPVPTSQIPDVHFFYKSSTATTSCLINGRSTA				SEQ ID 4
464	-----VAKMRCN-----				SEC10
	850	860	870	880	
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWE				SEQ ID 4
464	-----SAEACPLCTE-----				SEC10
	890	900	910	920	
879	HDFHEIEGACKRGFQETLYVWNEPKWCIKGISLPEKKLA				SEQ ID 4
464	-----T-----				SEC10
	930	940	950	960	
919	CETVDFWLKVGAvgafTAVLLVALTCYFWKKNQKLEYKY				SEQ ID 4
464	-----				SEC10
	970	980	990	1000	
959	SKLVMTTNSKECELPAADSCAIMEGEDNEEEVVYSNKQL				SEQ ID 4
464	-----S-----				SEC10
	1010	1020	1030		
999	LGKLKSLATKEKEDHFEESVQLKTSRSPNI.				SEQ ID 4
464	-----R-----				SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B